

## FIGURE 1

**Target segment starts with AA**  
**Target segment: 5' -> 3'**

	GC Ratio	Position	siRNA Sense strand: 5' -> 3' siRNA Antisense strand: 3' -> 5'
AATGTCCACATGTCAGGAGGC [SEQ ID NO:11]	0.52	93	UGUCCACAUUGUCAGGAGGCUU [SEQ ID NO:29] UUACAGGUGUACAGUCCUCCG [SEQ ID NO:47]
AACAAGACTGGACCATCCAGT [SEQ ID NO:12]	0.48	124	CAAGACUGGACCAUCCAGUUU [SEQ ID NO:30] UUGUUCUGACCUGGUAGGUCA [SEQ ID NO:48]
AAGTGCCTCCAGCACTATTGT [SEQ ID NO:13]	0.48	246	GUGCGUCCAGCACUAUUGUUU [SEQ ID NO:31] UUCACGCAGGUCGUGAUAAACA [SEQ ID NO:49]
AACCTCAAGATCCACAGCAGC [SEQ ID NO:14]	0.52	648	CCUCAAGAUCACAGCAGCUU [SEQ ID NO:32] UUGGAGUUCUAGGUGUCGUCG [SEQ ID NO:50]
AAGTACTGGATGTCTCAGACG [SEQ ID NO:15]	0.48	888	GUACUGGAUGUCUCAGACGUU [SEQ ID NO:33] UUCAUGACCUACAGAGUCUGC [SEQ ID NO:51]
AAGGTTAGTCCGGACAGAGTC [SEQ ID NO:16]	0.52	1037	GGUUAGUCCGGACAGAGUCUU [SEQ ID NO:34] UUCCAAUCAGGCCUGUCUCAG [SEQ ID NO:52]
AAGCCACCTCGCTATTCAGAC [SEQ ID NO:17]	0.52	1089	GCCACCUCGCUAUUCAGACUU [SEQ ID NO:35] UUCGGUGGGAGCGAUAGUCUG [SEQ ID NO:53]
AAGAACTTCAACCTGCCAGCA [SEQ ID NO:18]	0.48	1305	GAACUUCAACCUGCCAGCAUU [SEQ ID NO:36] UUCUUGAAGUUGGACGGUCGU [SEQ ID NO:54]
AACTTCAACCTGCCAGCATCC [SEQ ID NO:19]	0.52	1308	CUUCAACCUGCCAGCAUCCUU [SEQ ID NO:37] UUGAAGUUGGACGGUCGUAGG [SEQ ID NO:55]

AATTGAAGTGGAGCCAACGTC [SEQ ID NO:20]	0.48	1463	UUGAAGUGGAGCCAACGUCUU [SEQ ID NO:38] UUAACUUCACCUCGGUUGCAG [SEQ ID NO:56]
AACGTCGGAGAACATGAAGAGGT [SEQ ID NO:21]	0.48	1478	CGUCGGAGAACUGAAAGAGGUUU [SEQ ID NO:39] UUGCAGCCUCUACUUCUCCA [SEQ ID NO:57]
AAGAGTCAGAGGATGACTTCG [SEQ ID NO:22]	0.48	1513	GAGUCAGAGGAUGACUUCGUU [SEQ ID NO:40] UUCUCAGUCUCCUACUGAAGC [SEQ ID NO:58]
AACCAGGCAGATTGCTCAAGA [SEQ ID NO:23]	0.48	1922	CCAGGCAGAUUGCUCAGAUU [SEQ ID NO:41] UUGGUCCGUCUAACGAGUUCU [SEQ ID NO:59]
AACGTCTTCTATGACAACGGC [SEQ ID NO:24]	0.48	2007	CGUCUUCUAUGACAACGGCUU [SEQ ID NO:42] UUGCAGAAGAUACUGUUGCCG [SEQ ID NO:60]
AACTGCGCATCCAGAACGGCT [SEQ ID NO:25]	0.52	2098	CUGCGCAUCCAGAAUGGUUU [SEQ ID NO:43] UUGACCGUAGGUUCUACCGA [SEQ ID NO:61]
AATCTGGTATGAACCTCACGC [SEQ ID NO:26]	0.48	2222	UCUGGUUAUGAACUCCACGCCUU [SEQ ID NO:44] UUAGACCAUACUUGAGGUGCG [SEQ ID NO:62]
AACCTCAGCCAGATTGGCATG [SEQ ID NO:27]	0.52	2313	CCUCAGCCAGAUUGGCAUGUU [SEQ ID NO:45] UUGGAGUCGGUCUAACCGUAC [SEQ ID NO:63]
AAGAGAGACCTACCTCACCA [SEQ ID NO:28]	0.48	2383	GAGAGACCUACCUUCACCAUU [SEQ ID NO:46] UUCUCUCUGGAUGGAAGUGGU [SEQ ID NO:64]

**Target segment starts with CA**

Target segment: 5' -> 3'

GC Ratio Position siRNA Sense strand: 5' -> 3'  
siRNA Antisense strand: 3' -> 5'

CAGGAATGTCCACATGTCAGG [SEQ ID NO:65]	0.52	89	GGAAUGUCCACAUGUCAGGUU [SEQ ID NO:94] UUCCUUACAGGUGUACAGUCC [SEQ ID NO:123]
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CACATGTCAGGAGGCAACCTT [SEQ ID NO:66]	0.52	99	CAUGUCAGGAGGCAACCUUUU [SEQ ID NO:95] UUGUACAGGUCCUCCGUUGGAA [SEQ ID NO:124]
CAAGTGCCTCAGCACTATTG [SEQ ID NO:67]	0.52	245	AGUGCGUCCAGCACAUUUGUU [SEQ ID NO:96] UUUCACGCAGGUCGUGAUAAAC [SEQ ID NO:125]
CAGCACTATTGTCACACCAGC [SEQ ID NO:68]	0.52	255	GCACUAUUGUCACACCAGCUU [SEQ ID NO:97] UUCGUGAUAAACAGUGUGGUCG [SEQ ID NO:126]
CACACTGAGGCCAACTTCTCT [SEQ ID NO:69]	0.52	783	CACUGAGGCCAACUUCUCUUU [SEQ ID NO:98] UUGUGACUCCGGUUGAAGAGA [SEQ ID NO:127]
CAGAGATCTCGGCAACTCCAT [SEQ ID NO:70]	0.52	848	GAGAUCUCGGCAACUCCAUUU [SEQ ID NO:99] UUCUCUAGAGCCGUUGAGGUA [SEQ ID NO:128]
CAACTCCATCAAGCACAGGTT [SEQ ID NO:71]	0.48	860	ACUCCAUCAGCACAGGUUUU [SEQ ID NO:100] UUUGAGGUAGUUCGUGUCCAA [SEQ ID NO:129]
CACCAAGTACTGGATGTCTCA [SEQ ID NO:72]	0.48	884	CCAAGUACUGGAUGUCUCAUU [SEQ ID NO:101] UUGGUUCAUGACCUACAGAGU [SEQ ID NO:130]
CAAGTACTGGATGTCTCAGAC [SEQ ID NO:73]	0.48	887	AGUACUGGAUGUCUCAGACUU [SEQ ID NO:102] UUUCAUGACCUACAGAGUCUG [SEQ ID NO:131]
CATCTCTGATCATCCACCGA [SEQ ID NO:74]	0.48	1005	UCUUCUGAUCAUCCACCGAUU [SEQ ID NO:103] UUAGAAGACUAGUAGGUGGCU [SEQ ID NO:132]
CAAGGTTAGTCCGGACAGAGT [SEQ ID NO:75]	0.52	1036	AGGUUAGUCCGGACAGAGUUU [SEQ ID NO:104] UUUCCAAUCAGGCCUGUCUCA [SEQ ID NO:133]
CAGACCTGCACATCAGTCAGA [SEQ ID NO:76]	0.52	1105	GACCUGCACAUCAUCAGUCAGAUU [SEQ ID NO:105] UUCUGGACGUGUAGUCAGUCU [SEQ ID NO:134]

CACACGGCAGCAGAAGAACTT [SEQ ID NO:77]	0.52	1292	CACGGCAGCAGAAGAACUUUU [SEQ ID NO:106] UUGUGCCGUCGUUCUUGAA [SEQ ID NO:135]
CACGGCAGCAGAAGAACTTCA [SEQ ID NO:78]	0.52	1294	CGGCAGCAGAAGAACUUCAUU [SEQ ID NO:107] UUGCCGUCGUUCUUGAAGU [SEQ ID NO:136]
CAGCAGAAGAACCTCAACCTG [SEQ ID NO:79]	0.48	1299	GCAGAAGAACUUCAACCUGUU [SEQ ID NO:108] UUCGUCUUCUUGAAGUUGGAC [SEQ ID NO:137]
CAGAAGAACCTCAACCTGCCA [SEQ ID NO:80]	0.48	1302	GAAGAACUUCAACCUGCCAUU [SEQ ID NO:109] UUCUUCUUGAAGUUGGACGGU [SEQ ID NO:138]
CAACGTCGGAGAATGAAGAGGG [SEQ ID NO:81]	0.52	1477	ACGUCCGGAGAAUGAAGAGGUU [SEQ ID NO:110] UUUGCAGCCUCUUACUUCUCC [SEQ ID NO:139]
CATGATGAGGCCGAAGAGTCA [SEQ ID NO:82]	0.52	1500	UGAUGAGGCCGAAGAGUCAUU [SEQ ID NO:111] UUACUACUCCGGCUUCUCAGU [SEQ ID NO:140]
CAGAGGATGACTCGAGGAGA [SEQ ID NO:83]	0.52	1519	GAGGAUGACUUUCGAGGAGAUU [SEQ ID NO:112] UUCUCCUACUGAAGCUCCUCU [SEQ ID NO:141]
CAGACCAGCATTTCTTCAG [SEQ ID NO:84]	0.52	1587	GACCAGCAUCUCCUUCAGUU [SEQ ID NO:113] UUCUGGUCGUAGAAGGAAGUC [SEQ ID NO:142]
CAGCATCTTCCTTCAGGAGTG [SEQ ID NO:85]	0.52	1592	GCAUCUCCUUCAGGAGUGUU [SEQ ID NO:114] UUCGUAGAAGGAAGUCCUCAC [SEQ ID NO:143]
CATCCGGCTGATTGACATTGA [SEQ ID NO:86]	0.48	1706	UCCGGCUGAUUGACAUUGAUU [SEQ ID NO:115] UUAGGCCGACUAACUGUAACU [SEQ ID NO:144]
CATCATCACCAAGCCTCTGTAA [SEQ ID NO:87]	0.48	1844	UCAUCACCAGCCUCUGUAUU [SEQ ID NO:116] UUAGUAGUGGUUCGGAGACAUU [SEQ ID NO:145]

CATCCAGAATGGCTGGCTATG [SEQ ID NO:88]	0.52	2105	UCCAGAAUGGCUGGCUAUGUU [SEQ ID NO:117] UUAGGUUUACCGACCGAUAC [SEQ ID NO:146]
CAATCTGGTATGAACCTCCACG [SEQ ID NO:89]	0.48	2221	AUCUGGUUAUGAACUCCACGUU [SEQ ID NO:118] UUUAGACCAUACUUGAGGUGC [SEQ ID NO:147]
CAACCAGCAGAGGAATAATC [SEQ ID NO:90]	0.48	2265	ACCAGCAGAGGCAAUAUCUU [SEQ ID NO:119] UUUGGUCGUCUCCGUUAUUAG [SEQ ID NO:148]
CAGCAGAGGCAATAATCTGGC [SEQ ID NO:91]	0.52	2269	GCAGAGGCAAUAUCUGGUU [SEQ ID NO:120] UUCGUCUCCGUUAUUAGACCG [SEQ ID NO:149]
CAACCTCAGCCAGATTGGCAT [SEQ ID NO:92]	0.52	2312	ACCUCAGCCAGAUUGGCAUUU [SEQ ID NO:121] UUUGGAGUCGGUCUAACCGUA [SEQ ID NO:150]
CAAGAAGAGAGACCTACCTTC [SEQ ID NO:93]	0.48	2379	AGAAGAGAGACCUACCUUCUU [SEQ ID NO:122] UUUCUUCUCUGGAUGGAAAG [SEQ ID NO:151]

**Target segment starts with GA**

Target segment: 5' -> 3'

	GC Ratio	Position	siRNA Sense strand: 5' -> 3' siRNA Antisense strand: 3' -> 5'
GAATGTCCACATGTCAGGAGG [SEQ ID NO:152]	0.52	92	AUGUCCACAUGUCAGGAGGUU [SEQ ID NO:181] UUUACAGGUGUACAGUCCUCC [SEQ ID NO:210]
GAAGAAGAACAAAGCTGAAGCC [SEQ ID NO:153]	0.48	476	AGAAGAACAAAGCUGAAGCCUU [SEQ ID NO:182] UUUCUUUCUGUUCGACUUCGG [SEQ ID NO:211]
GAACCTCAAGATCCACAGCAG [SEQ ID NO:154]	0.52	647	ACCUCAAGAACCCACAGCAGUU [SEQ ID NO:183] UUUGGAGUUCUAGGUGUCGUC [SEQ ID NO:212]
GAGATCTGGCAACTCCATCA [SEQ ID NO:155]	0.52	850	GAUCUCGGCAACUCCAUCUU [SEQ ID NO:184] UUCUAGAGCCGUUGAGGUAGU [SEQ ID NO:213]

GATCTCGGCAACTCCATCAAG [SEQ ID NO:156]	0.52	852	UCUCGGCAACUCCAUCAGUU [SEQ ID NO:185] UUAGAGCCGUUGAGGUAGUUC [SEQ ID NO:214]
GATGTCTCAGACGTGCACAGT [SEQ ID NO:157]	0.52	896	UGUCUCAGACGUGCACAGUUU [SEQ ID NO:186] UUACAGAGUCUGCACGUGUCA [SEQ ID NO:215]
GAGGAGATCCAGCAAGGTTAG [SEQ ID NO:158]	0.52	1024	GGAGAUCCAGCAAGGUUAGUU [SEQ ID NO:187] UUCUCUAGGUCGUUCCAAUC [SEQ ID NO:216]
GAGATCCAGCAAGGTTAGTCC [SEQ ID NO:159]	0.52	1027	GAUCCAGCAAGGUUAGGUUU [SEQ ID NO:188] UUCUAGGUCGUUCCAAUCAGG [SEQ ID NO:217]
GAAGCCACCTCGCTATTAGA [SEQ ID NO:160]	0.52	1088	AGCCACCUCGCUAUUCAGAUU [SEQ ID NO:189] UUUCGGUGGAGCGAUAGUCU [SEQ ID NO:218]
GAAGAACTTAACCTGCCAGC [SEQ ID NO:161]	0.52	1304	AGAACUUCAACCUGCCAGCUU [SEQ ID NO:190] UUUCUUGAAGUUGGACGGUCG [SEQ ID NO:219]
GAACCTAACCTGCCAGCATC [SEQ ID NO:162]	0.52	1307	ACUUCAACCUGCCAGCAUCUU [SEQ ID NO:191] UUUGAAGUUGGACGGUCGUAG [SEQ ID NO:220]
GACCTCGAACATCCAATCTTGGA [SEQ ID NO:163]	0.48	1424	CCUCGAAUCCAAUCUUGGAUU [SEQ ID NO:192] UUGGAGCUUAGGUAGAACCU [SEQ ID NO:221]
GAGCCAACGTCGGAGAATGAA [SEQ ID NO:164]	0.52	1473	GCCAACGUCGGAGAAUGAAUU [SEQ ID NO:193] UUCGGUUGCAGCCUCUUACUU [SEQ ID NO:222]
GAAGAGTCAGAGGATGACTTC [SEQ ID NO:165]	0.48	1512	AGAGUCAGAGGAUGACUUCUU [SEQ ID NO:194] UUUCUCAGUCUCCUACUGAAG [SEQ ID NO:223]
GAGTCAGAGGATGACTTCGAG [SEQ ID NO:166]	0.52	1515	GUCAGAGGAUGACUUCGAGUU [SEQ ID NO:195] UUCAGUCUCCUACUGAAGCUC [SEQ ID NO:224]

GAGGATGACTTCGAGGAGATG [SEQ ID NO:167]	0.52	1521	GGAUGACUUCGAGGAGAUGUU [SEQ ID NO:196] UUCCUACUGAAGCUCCUCUAC [SEQ ID NO:225]
GATGACTTCGAGGAGATGAAC [SEQ ID NO:168]	0.48	1524	UGACUUUCGAGGAGAUGAACUU [SEQ ID NO:197] UUACUGAAGCUCCUCUACUUG [SEQ ID NO:226]
GAATCGAGGAGATGAACCTG [SEQ ID NO:169]	0.52	1527	CUUCGAGGAGAUGAACCUUU [SEQ ID NO:198] UUGAAGCUCCUCUACUUGGAC [SEQ ID NO:227]
GACCAGCATCTTCCTTCAGGA [SEQ ID NO:170]	0.52	1589	CCAGCAUCUUCUUCAGGAUU [SEQ ID NO:199] UUGGUCGUAGAAGGAAGGUCCU [SEQ ID NO:228]
GACGCTCTATTCCGTTGTGAG [SEQ ID NO:171]	0.52	1871	CGCUCUAUUCGUUGUGAGUU [SEQ ID NO:200] UUGCGAGAUAGGCAACACUC [SEQ ID NO:229]
GAATCCTACACAAGGACCTCA [SEQ ID NO:172]	0.48	1978	AUCCUACACAAGGACCUAUU [SEQ ID NO:201] UUUAGGAUGUGUUCCUGGAGU [SEQ ID NO:230]
GAACGTCTTCTATGACAACGG [SEQ ID NO:173]	0.48	2006	ACGUCUUCUAUGACAACGGUU [SEQ ID NO:202] UUUGCAGAAGAUACUGUUGCC [SEQ ID NO:231]
GACACAGAGGAGGATAAGCTC [SEQ ID NO:174]	0.52	2163	CACAGAGGAGGAAAGCUCUU [SEQ ID NO:203] UUGUGUCUCCUCUAAUCGAG [SEQ ID NO:232]
GACATTCTTCTCTTGCTGG [SEQ ID NO:175]	0.48	2349	CAUUCUUCUUCUGCUGGUU [SEQ ID NO:204] UUGUAAGAAGAGAAAGACGACC [SEQ ID NO:233]
GAACAAGAAGAGAGACCTACC [SEQ ID NO:176]	0.48	2376	ACAAGAAGAGAGACCUACC [SEQ ID NO:205] UUUGUUUCUUCUCUGGAUGG [SEQ ID NO:234]
GAAGAGAGACCTACCTTCACC [SEQ ID NO:177]	0.52	2382	AGAGAGACCUACCUUCACCUU [SEQ ID NO:206] UUUCUCUCUGGAUGGAAGUGG [SEQ ID NO:235]

GAGAGACCTACCTCACCAAG [SEQ ID NO:178]	0.52	2385	GAGACCUACCUUCACCAAGUU [SEQ ID NO:207] UUCUCUGGAUGGAAGUGGUUC [SEQ ID NO:236]
GAGACCTACCTCACCAAGCT [SEQ ID NO:179]	0.52	2387	GACCUACCUUCACCAAGCUUU [SEQ ID NO:208] UUCUGGAUGGAAGUGGUUCGA [SEQ ID NO:237]
GACCTACCTCACCAAGCTCA [SEQ ID NO:180]	0.52	2389	CCUACCUUCACCAAGCUCAUU [SEQ ID NO:209] UUGGAUGGAAGUGGUUCGAGU [SEQ ID NO:238]

**Target segment starts with TA**

Target segment: 5' -> 3'

	GC Ratio	Position	siRNA Sense strand: 5' -> 3' siRNA Antisense strand: 3' -> 5'
TACTGGATGTCTCAGACGTGC [SEQ ID NO:239]	0.52	891	CUGGAUGUCUCAGACGUGCUU [SEQ ID NO:242] UUGACCUACAGAGUCUGCACG [SEQ ID NO:245]
TACGGAAGCCACCTCGCTATT [SEQ ID NO:240]	0.52	1084	CGGAAGGCCACCUCGCUAUUUU [SEQ ID NO:243] UUGCCUUCGGUGGGAGCGAUAA [SEQ ID NO:246]
TACCTTCACCAAGCTCATGGA [SEQ ID NO:241]	0.48	2393	CCUUCACCAAGCUCAUUGGAUU [SEQ ID NO:244] UUGGAAGUGGUUCGAGUACCU [SEQ ID NO:247]

## FIGURE 2

CLUSTAL W multiple sequence alignment results

MSF: 1005 Type: P Check: 5073

Name: hksr-1\_full\_cae84534\_1.pep oo Len: 1005 Check: 4093 Weight: 12.1  
 Name: mksr-1\_np\_038599.pep oo Len: 1005 Check: 1555 Weight: 12.7  
 Name: hksr-1\_partial\_aac50354\_1.pep oo Len: 1005 Check: 10 Weight: 10.7  
 Name: hksr-2\_aaq24226\_1.pep oo Len: 1005 Check: 732 Weight: 13.8  
 Name: mksr-2.pep oo Len: 1005 Check: 2473 Weight: 13.6  
 Name: dmksr\_np\_524236.pep oo Len: 1005 Check: 4070 Weight: 36.8  
 Name: ceksr\_aaa92436\_1.pep oo Len: 1005 Check: 2140 Weight: 26.8

	CA1	
	1	
hKSR-1(full)	MDRAALRAAA MGEKKEGGGG GDAAAEGGA GAAASRALQQ CGQLQKLIDI	
mKSR-1	MDRAALRAAA MGEKKEGGGG G..AAADGGA GAAVSRALQQ CGQLQKLIDI	
hKSR-1(partial).....	.....	.....
hKSR-2	.....	.....
mKSR-2	.....	.....
DmKSR	..... MS SNNNAPASAP DTGSTNANDP ISGSLSVDSN LVIIQDMIDL	
CeKSR	.....	.....
	50	
	CA1	
	51	100
hKSR-1(full)	SIGSLRGLRT KCAVSNDLTQ QEIRTEAKL VRYICKQRQC KLSVAPGERT	
mKSR-1	SIGSLRGLRT KCSVNDLTQ QEIRTEAKL VKYICKQQQS KLSVTPSDRT	
hKSR-1(partial).....	.....	.....
hKSR-2	..... MT DEQVCETVEK YGANREECAR LNALSCLRN VHMSGGNLSK	
mKSR-2	..... MT DEQVCETVEK YGANQEECAR LNALSCLRN VHKGNNLSK	
DmKSR	SANHLEGLRT QCAISSTLTQ QEIRCLESKL VRYFSELLLA KMRLNERIPA	
CeKSR	.....	.....
	101	150
hKSR-1(full)	PELNSYPRFS DWLYTFNVRP EVV....QEI PRDLTLDALL EMNEAKVKET	
mKSR-1	AELNSYPRFS DWLYIFNVRP EVV....QEI PQELTLDALL EMDEAKAKEM	
hKSR-1(partial).....	.....	.....
hKSR-2	QDWTIQWPTT ETGKENNPVC PPE....PTP WIRTHLSQSP RVPSKCVQHY	
mKSR-2	QDWIIQWPTT EPGQESNPVC PPE....PSP WIRTHLSQSP RVQTKCPQHF	
DmKSR	NGLVPHTTGN ELRQWLRRVVG LSQGTLTACL ARLTTLEQLS RLSDEEIRQL	
CeKSR	.....	.....
	151	200
hKSR-1(full)	LRRCGASGDE ..... CGRL QYALTCLRKV TGLGGEHKED SSWSSLDARR	
mKSR-1	LRRWGASTEE ..... CSRL QQALTCLRKV TGLGGEHKMD SGWSSTDARD	
hKSR-1(partial).....	.....	.....
hKSR-2	CHTSPTPGAP ..... VYTH VDRLTVDAYP GLC PPPP.LE SGHRS LPPSP	
mKSR-2	CPTSPTPGTP ..... VYTQ VDRLTVDAYP NLC PPPP PLE SGHRS LPPSP	
DmKSR	LADSPSQREE EELRRLTRAM QNLRKCMESL ESGTAASNND PEQWHWDSDWD	
CeKSR	..... MM QTQVASRAGY SNLPQFGAGI AQDIKTQAIN	

## CA2

201

250

hKSR-1(full) ESGSGPSTD T LSAASLPWPP GSSQLGRAGN SAQGPRSI SV SALPASDSPT  
 mKSR-1 SSLG..... PPMD MLSSLGRAGA STQGPRSI SV SALPASDSPV  
 hKSR-1(partial) ..  
 hKSR-2 RQRHAVRTPP RTPNIVTTVT PPGTPPMRKK NKLKPPGTTP PSSRKLIHLI  
 mKSR-2 RQRHVVRTPP RTPNIVTTVT PPGTPPMRKK NKLKPPGTTP PSSRKLIHLI  
 DmKSR RPTHIHRGSV GNIGLGNNST ASPRTHHRQH GVKGKNSALA NSTNFKSGRQ  
 CeKSR NLKECLKLTT INRFLTSSYE EDAKSVERKI FSAVYQMTKI GLIDREKREI

251

300

hKSR-1(full) PSFSEGLSDT CIPLHASGRL TPRALHSFIT PPTTPQLRRH TKLKPPRTTP  
 mKSR-1 PGLSEGLSDS CIPLHTSGRL TPRALHSFIT PPTTPQLRRH AKLKPPRTTP  
 hKSR-1(partial) .. EFRHTSAL TQHTAHTQHT SAHTQHSFIT PPTTPQLRRH TKLKPPRTTP  
 hKSR-2 PGFTALHRSK SHEFQLGHGV DEAHTPKAKK KSKPLNLKIH SSVGSCENIP  
 mKSR-2 PGFTALHRSK SHEFQLGNRV DEANTPKAKK KSKPLNLKIH SSVGSCENIP  
 DmKSR SPSATEELNS TQGSQTLTLL TPSPPNSPFT PSSGLSSSLN GTPQRSRGTP  
 CeKSR NAIWFTFVGL SAQNIRHLEI CSITDFNALF SITNQELRSL ADRGRLDVET

301

350

hKSR-1(full) PPSRK..... VFQ LLPSFPTLTR SKSHESQLGN  
 mKSR-1 PPSRK..... VFQ LLPSFPTLTR SKSHESQLGN  
 hKSR-1(partial) PPSRK..... VFQ LLPSFPTLTR SKSHESQLGN  
 hKSR-2 SQQRSP... LSER SLRSFFVGHA PFLPSTPPVH  
 mKSR-2 AQQRSP... LSER SLRSFFVGHG PFLPSTPPVH  
 DmKSR PPARKHQTL SQSHVQVDGE QLARNRLPTD PSPDSHSSTS SDIFVDPNTN  
 CeKSR KRKLQS... TVILQN HWNAYHSRTS SGSTDDEPSGQ

## CA3

351

400

hKSR-1(full) RIDDVSSMRF DLHGSPQMV RRDIGLSVTH RFSTKSWLSQ VCHVCQKSMI  
 mKSR-1 RIDDVTPMKF ELPHGSPQLV RRDIGLSVTH RFSTKSWLSQ VCNVCQKSMI  
 hKSR-1(partial) RIDDVSSMRF DLHGSPQMV RRDIGLSVTH RFSTKSWLSQ VCHVCQKSMI  
 hKSR-2 TEANFSANTL SVPRWSPQIP RRDLGNSIKH RFSTKYWMSQ TCTVCGKGML  
 mKSR-2 TEANFSANTL SVPRWSPQIP RRDLGNSIKH RFSTKYWMSQ TCTVCGKGML  
 DmKSR ASSGGSSSNV LMVPCSPGVG HVGMGHAIKH RFTKALGFMA TCTLCKQVF  
 CeKSR STPAIVTPSP KFNVPSSLVT SAKMIQSSSM GFATTPKSPK TSSRLVHAIP

## CA3

401

450

hKSR-1(full) FG.VKCKHCR LKCHNKCTKE APACRISFLP ... LTRLRR. ....  
 mKSR-1 FG.VKCKHCR LKCHNKCTKE APACRITFLP ... LARLRR. ....  
 hKSR-1(partial) FG.VKCKHCR LKCHNKCTKE APACRISFLP ... LTRLRR. ....  
 hKSR-2 FG.LKCKNCK LKCHNKCTKE APPCHLLIIH RGDPARLVR. ....  
 mKSR-2 FG.LKCKNCK LKCHNKCTKE APPCHLLIIH RGDPARLVR. ....  
 DmKSR HRWMKTDCK YICHKSCAPH VPPSCGLPRE YVDEFRIKE QGGYASLPHV  
 CeKSR HKWHRSTKFR FSGDAVCHFC QRPLGFGFLN AWEKCRSCKW KVHTQCKGRV

CA4

451

500

hKSR-1(full) ... TESVPSD INNPVDRAAE PHFGTLKPAL TKK.... EH PPAMNHLDSS  
 mKSR-1 ... TESVPSD INNPVDRAAE PHFGTLKPAL TKK.... EH PPAMN.LDSS  
 hKSR-1(partial) ... TESVPSD INNPVDRAAE PHFGTLKPAL TKK.... EH PPAMNHLDSS  
 hKSR-2 ... TESVPCD INNPLRKPPR YSDLHISQTL PTKTNKINKDH IPVPYQPDSS  
 mKSR-2 ... TESVPCD INNPVRKPAR YSDLHISQTL PTKTNKINKDH IPVPYQPDSS  
 DmKSR HGAAGKSPLV KKSTLGKPLH QQHGDSSSPS SSCTSSTPSS PALFQQRERE  
 CeKSR GDSCGLTPDH LRFLFDKLIQ ENNGGMWKDP QSVPGRSRSMN EPAFQFPDTA

**CA4**

	501	550
hKSR-1 (full)	SNPSSTTSST PSSPAPFPTS SNPSSATTP.	.....
mKSR-1	SNPSSTTSST PSSPAPFLTS SNPSSATTP.	.....
hKSR-1 (partial)	SNPSSTTSST PSSPAPFPTS SNPSSATTP.	.....
hKSR-2	SNPSSTTSST PSSPAPPLPP SATPPSPLH.	.....
mKSR-2	SNPSSTTSST PSSPAPPLPP SATPPSPLH.	.....
DmKSR	LDQAGSSSA NLLPTPSLGK HQPSQFNFPN VTVTSSGGSG GVSLISNEPV	
CeKSR	IDSSSTNSS APSTPALPAG ISGNVSSLTA PYR.....	.....SERK

**CA4**

	551	600
hKSR-1 (full)	....PNPSPG QRDSRFNFP AYFIHHRQQF IFPDISAFAH AAPLPEAADG	
mKSR-1	....PNPSPG QRDS..... RF SFPDISACSQ AAPLSSTADS	
hKSR-1 (partial)	....PNPSPG QRDSRFNFP AYFIHHRQQF IFPDISAFAH AAPLPEAADG	
hKSR-2	....PSPQCT RQQKNFNLP SHYYKYKQQF IFPDVVPVPE TPTRAPQVIL	
mKSR-2	....PSPQCP RQKKNFNLP SHYYKYKQQF IFPDVVPVPE TPTRAPQVIL	
DmKSR	PEQFPTAPAT ANGGLDSLVS SSNGHMSSI GSQTNSASTA ATLTGSLVNS	
CeKSR	FLFPDTENYS VHNRLPILVI SEGDHPTTTE IQQETENHNK SAAASMSGNI	

	601	650
hKSR-1 (full)	TRLDDQPKAD VLEAHEAEAE EPEAGKSEAE DDE .DEVDDL PSSRRPWRG.	
mKSR-1	TRLDDQPKTD VLGVHEAEAE EPEAGKSEAE DDEEDEVDDL PSSRRPWRG.	
hKSR-1 (partial)	TRLDDQPKAD VLEAHEAEAE EPEAGKSEAE DDE .DEVDDL PSSRRPWRG.	
hKSR-2	HPTVTSNPILE GNPLLQIEVE PTSENEEVHD EAEESEDDFE EMNLSSAR	
mKSR-2	HPTVTSNTILE GNPLLQIEVE PTSENEESHN EAESEDEFE EMNLSSAR	
DmKSR	TTTTSTCSFF PRKLSTAGVD KRTPTSECT DTHKSNDSDK TVSLGSAST	
CeKSR	ESEGTVANH EDSTGSQEVD SEAAPSQEAV DKFNKRADGG FTWERHAWN	M

	651	CA5 700
hKSR-1 (full)	PISRKAS... .... .QTSVYLQEW DIPFEQVELG EPIGQGRWGR	
mKSR-1	PISRKAS... .... .QTSVYLQEW DIPFEQVELG EPIGQGRWGR	
hKSR-1 (partial)	PISRKAS... .... .QTSVYLQEW DIPFEQVELG EPIGQGRWGR	
hKSR-2	SFPRKAS... .... .QTSIFLQEW DIPFEQLEIG ELIGKGRFGQ	
mKSR-2	SFPRKAS... .... .QTSIFLQEW DIPFEQLEIG ELIGKGRFGQ	
DmKSR	DSDRTPVRVD STEDGDSQW RQNSISLKEW DIPYGDLLL ERIGQGRFGT	
CeKSR	STIRGPN... .... A QASNEVTIQ FETIEFDKQA PIIGRGRFGK	

**CA5**

	701	750
hKSR-1 (full)	VHRGRWHGEV AIRLLEM.D.G HNQDH.LKLF KKEVMNYRQT RHENVVLFMG	
mKSR-1	VHRGRWHGEV AIRLLEM.D.G HNQDH.LKLF KKEVMNYRQT RHENVVLFMG	
hKSR-1 (partial)	VHRGRWHGEV AIRLLEM.D.G HNQDH.LKLF KKEVMNYRQT RHENVVLFMG	
hKSR-2	YHGRWHGEV AIRLIDIE.R DNEDQ.LKAF KREVMAYRQT RHENVVLFMG	
mKSR-2	YHGRWHGEV AIRLIDIE.R DNEDQ.LKAF KREVMAYRQT RHENVVLFMG	
DmKSR	VHRALWHGDV AVKLLNEDYL QDEHM.LETF RSEVANFKNT RHENLVLFMG	
CeKSR	VLRGFHGYDV AVKVYTMEHI SDASKKAEEF KLEVSAYKNT RHDNIALFLG	

**CA5**

	751	800
hKSR-1 (full)	ACMNPPHLAI ITSFCKG.RT LHSFVRDPKT SLDINKTRQI AQEIICKGMGY	
mKSR-1	ACMNPPHLAI ITSFCKG.RT LHSFVRDPKT SLDINKTRQI AQEIICKGMGY	
hKSR-1 (partial)	ACMNPPHLAI ITSFCKG.RT LHSFVRDPKT SLDINKTRQI AQEIICKGMGY	
hKSR-2	ACMSPPHLAI ITSLCKG.RT LYSVVRDAKI VLDVNKTRQI AQEIVKGMGY	
mKSR-2	ACMSPPHLAI ITSLCKG.RT LYSVVRDAKI VLDVNKTRQI AQEIVKGMGY	
DmKSR	ACMNPPYLAI VTSLCKG.NT LYTYIHQRRE KFAMNRTLLI AQQIAQGMGY	
CeKSR	YFMSDGQYGM VMSLSKGSQS LYTLLHVRE KLDLATRKI AQQICQAVSY	

**CA5**

	801	850
hKSR-1 (full)	LHAKGIVHKD LKSKNVFYDN GKVVITDFGL FGISGVVREG RRENQLKLSH	
mKSR-1	LHAKGIVHKD LKSKNVFYDN GKVVITDFGL FGISGVVREE RRENQLKLSH	
hKSR-1 (partial)	LHAKGIVHKD LKSKNVFYDN GKVVITDFGL FGISGVVREG RRENQLKLSH	
hKSR-2	LHAKGILHKD LKSKNVFYDN GKVVITDFGL FSISGVLQAG RREDKLRIQN	
mKSR-2	LHAKGILHKD LKSKNVFYDN GKVVITDFGL FSISGVLQAG RRDDKLRIQN	
DmKSR	LHAREIIHKD LRTKNIFIEN GKVIITDFGL FSSTKLLYCD MG... LGVPH	
CeKSR	LHTKKILHKD LRSKNILLES KNKVVITDFG ILSMKRLAHP KQKSGYLTSK	

**CA5**

	851	900
hKSR-1 (full)	DWLCYLAPEI VREMTPGKDE ... DQLPFSK AADVYAFGTW WYELQARDWP	
mKSR-1	DWLCYLAPEI VREMIPGRDE ... DQLPFSK AADVYAFGTW WYELQARDWP	
hKSR-1 (partial)	DWLCYLAPEI VREMTPGKDE ... DQLPFSK AADVYAFGTW WYELQARDWP	
hKSR-2	GWLCHLAPEI IRQLSPDTEE ... DKLPFSK HSDVFALGTT WYELHAREWP	
mKSR-2	GWLCHLAPEI IRQLSPDTEE ... DKLPFSK HSDVFALGTT WYELHAREWP	
DmKSR	NWLCYLAPEL IRALQPEKPR G.. ECLEFTP YSDVYSFGTV WYELICGEFT	
CeKSR	FWTNYIAPEL AMAMRTEYDE YECDDFPFSE NSDVYAFGCV WFEMLTGALP	

**CA5**

	901	950
hKSR-1 (full)	LKNQAAEASI WQIGSGEGMK RVLTSVSLGK EVSEILSACW AFDLQERPSF	
mKSR-1	FKHQPAEALI WQIGSGEGVW RVLASVSLGK EVGEILSACW AFDLQERPSF	
hKSR-1 (partial)	LKNQAAEASI WQIGSGEGMK RVLTSVSLGK EVSEILSACW AFDLQERPSF	
hKSR-2	FKTQPAEAI WQMGTG.. MK PNLSQIGMGK EISDILLFCW AFEQEERPTF	
mKSR-2	FKTQPAEAI WQMGTG.. MK PNLSQIGMGK EISDILLFCW AFEQEERPTF	
DmKSR	FKDQPAESII WQVGRG.. MK QSLANLQSGR DVKDMLLCW TYEKHRPQF	
CeKSR	YAGELPHQIL FAKTQG.. IR PVLPNVKCTQ ELKELLVSCW NTAPQDRPTL	

**CA5**

	951	1000
hKSR-1 (full)	SLLMDMLEKL PK.. LNRRRLS HPGHFWKSAD INSSKVVPRF ERFGLGVLES	
mKSR-1	SLLMDMLERL PK.. LNRRRLS HPGHFWKSAD INSSKVMRPF ERFGLGTLES	
hKSR-1 (partial)	SLLMDMLEKL PK.. LNRRRLS HPGHFWKSAE L..... . . . . .	
hKSR-2	TKLMDMLEKL PK.. RNRRRLS HPGHFWKSAE L..... . . . . .	
mKSR-2	TKLMDMLEKL PK.. RNRRRLS HPGHFWKSAE L..... . . . . .	
DmKSR	ARLLSLLLEHL PKKRLARSPS HPVNLSRSAE SVF..... . . . . .	
CeKSR	TDINLKLTAL PKKPRVNRSP SFPVMMKSYE STF..... . . . . .	

**1001**

hKSR-1 (full)	SNPKM
mKSR-1	GNPKM
hKSR-1 (partial)	.....
hKSR-2	.....
mKSR-2	.....
DmKSR	.....
CeKSR	.....